

WEST Search History

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DATE: Monday, April 25, 2005

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
		<i>DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L12	L11 AND L9	65
<input type="checkbox"/>	L11	L10 AND L3	261
<input type="checkbox"/>	L10	l2 AND L1	997
<input type="checkbox"/>	L9	L8 or l7	26517
<input type="checkbox"/>	L8	(435/7.1,7.23)![CCLS]	11848
<input type="checkbox"/>	L7	(530/350)![CCLS]	16625
<input type="checkbox"/>	L6	(530)![CCLS]	0
<input type="checkbox"/>	L5	(530)![CCLS]	0
<input type="checkbox"/>	L4	84P2A9	0
<input type="checkbox"/>	L3	prostate	33051
<input type="checkbox"/>	L2	tumor\$ or tumuor\$ or cancer\$ or neoplas\$	161183
<input type="checkbox"/>	L1	(jakobovits or afar or challita\$ or levin or mitchell or hubert).in.	32792

END OF SEARCH HISTORY

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 3, 2005, 05:44:40 ; Search time 174.5 Seconds
(without alignments)
10394.878 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 4167
Sequence: 1 attcggcaccgaggtggaagt.....accaaaaaaaaaaaaaaaaaa 2345

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103618_22701/app_query.fasta_1.2
503

-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312_@CGN_1_1_242_@runat_01042005_103618_22701 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	2826	67.8	528	4	AAB92632 Human pro
2	2826	67.8	528	5	Abb97288 Novel hum
3	2694	64.7	504	4	Aau06524 Prostate
4	1940	46.6	376	8	Adr99239 Hypotheti
5	1202	28.8	313	4	Abg08002 Novel hum
6	608.5	14.6	423	4	Abg23408 Novel hum
7	591.5	14.2	446	5	Abb75706 Human pho
8	588.5	14.1	482	5	Abp43772 14 clone
9	533.5	12.8	453	5	Abb97561 Novel hum
10	530.5	12.7	351	4	Aab94662 Human pro
11	530.5	12.7	351	5	Abb97470 Novel hum
12	338	8.1	275	4	Aab92468 Human pro
13	320.5	7.7	223	4	Aam15386 Peptide #
14	320.5	7.7	223	4	Abb34392 Peptide #
15	320.5	7.7	223	4	Aam27874 Peptide #
16	320.5	7.7	223	4	Abb29229 Peptide #
17	320.5	7.7	223	4	Aam67577 Human bon
18	320.5	7.7	223	4	Aam55182 Human bra
19	320.5	7.7	223	4	Abg49223 Human liv
20	320.5	7.7	223	4	Aam03148 Peptide #
21	320.5	7.7	223	5	Abg37168 Human pep
22	320.5	7.7	223	8	Abo59933 Human gen
23	236.5	5.7	123	4	Aam95677 Human rep
24	198	4.8	1038	7	Adc03412 Rice flow
25	169.5	4.1	554	3	Aag36165 Arabidops
26	169.5	4.1	652	3	Aag36164 Arabidops
27	169.5	4.1	781	3	Aag36163 Arabidops
28	169	4.1	767	6	Abr53431 Protein s
29	169	4.1	767	7	Adk64670 Disease t
30	162.5	3.9	815	5	Aag78388 Human H37
31	162.5	3.9	815	7	Aae38620 Human H37
32	162.5	3.9	815	7	Aae38621 Human H37
33	162.5	3.9	815	8	Adp23184 PRO polyp
34	162	3.9	381	2	Aay07056 Renal can
35	159.5	3.8	573	4	Adm19760 Protein e
36	158.5	3.8	962	4	Abg04842 Novel hum
37	158.5	3.8	1403	8	Adh09502 Human hos
38	158.5	3.8	1462	6	Abp58346 Human cel
39	158.5	3.8	1462	6	Abu05132 Human exp
40	158.5	3.8	1462	6	Abu05136 Human exp
41	158.5	3.8	1462	6	Abu05131 Human exp
42	158.5	3.8	1462	6	Abu05135 Human exp
43	158.5	3.8	1462	7	Adj68950 Human hea
44	158.5	3.8	1462	8	Adh09503 Human hos
45	158.5	3.8	1462	8	Adp55142 Human PRO

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 3, 2005, 08:28:10 ; Search time 37.5 Seconds
(without alignments)
9336.110 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 4167
Sequence: 1 attcggcacgaggtggaagt.....accaaaaaaaaaaaaaaaaaaa 2345

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103620_22743/app_query.fasta_1.2
503

-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312_@CGN_1_1_46_@runat_01042005_103620_22743 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	666	16.0	124	4	US-09-621-976-4580	Sequence 4580, Ap
2	162.5	3.9	815	4	US-09-538-092-1196	Sequence 1196, Ap
3	158.5	3.8	1462	4	US-09-538-092-1043	Sequence 1043, Ap
4	156	3.7	929	4	US-09-538-092-1232	Sequence 1232, Ap
5	154.5	3.7	620	4	US-09-270-767-46214	Sequence 46214, A
6	147.5	3.5	362	4	US-09-270-767-42306	Sequence 42306, A
7	139	3.3	788	3	US-08-630-915A-30	Sequence 30, Appl
8	139	3.3	788	4	US-09-879-957-30	Sequence 30, Appl
9	133.5	3.2	1564	4	US-10-144-198-2	Sequence 2, Appli
10	133.5	3.2	1564	4	US-10-144-198-4	Sequence 4, Appli
11	133	3.2	664	1	US-08-421-661-6	Sequence 6, Appli
12	129	3.1	1034	4	US-09-976-594-590	Sequence 590, App
13	127.5	3.1	748	3	US-08-725-459B-24	Sequence 24, Appl
14	127	3.0	709	4	US-09-949-016-10367	Sequence 10367, A
15	126.5	3.0	1402	4	US-09-248-796A-14503	Sequence 14503, A
16	126	3.0	598	4	US-09-538-092-1083	Sequence 1083, Ap
17	126	3.0	664	4	US-09-917-254-78	Sequence 78, Appl
18	126	3.0	1400	4	US-09-764-176-7	Sequence 7, Appli
19	123	3.0	971	4	US-09-538-092-1332	Sequence 1332, Ap
20	122.5	2.9	621	4	US-09-248-796A-15807	Sequence 15807, A
21	122.5	2.9	976	3	US-09-302-812-4	Sequence 4, Appli
22	122.5	2.9	976	3	US-09-511-477-4	Sequence 4, Appli
23	122.5	2.9	976	3	US-09-511-507-4	Sequence 4, Appli
24	122	2.9	968	3	US-09-302-812-6	Sequence 6, Appli
25	122	2.9	968	3	US-09-511-477-6	Sequence 6, Appli
26	122	2.9	968	3	US-09-511-507-6	Sequence 6, Appli
27	121	2.9	733	3	US-08-725-459B-21	Sequence 21, Appl
28	121	2.9	769	3	US-08-725-459B-39	Sequence 39, Appl
29	120.5	2.9	1992	4	US-09-538-092-1327	Sequence 1327, Ap
30	120	2.9	769	3	US-08-725-459B-37	Sequence 37, Appl
31	120	2.9	769	3	US-08-725-459B-38	Sequence 38, Appl
32	120	2.9	769	3	US-08-725-459B-40	Sequence 40, Appl
33	120	2.9	1739	4	US-09-976-594-76	Sequence 76, Appl
34	120	2.9	1739	4	US-09-538-092-824	Sequence 824, App
35	120	2.9	1740	4	US-09-949-016-8860	Sequence 8860, Ap
36	119.5	2.9	1589	4	US-09-543-681A-4998	Sequence 4998, Ap
37	119.5	2.9	2842	1	US-07-741-940-7	Sequence 7, Appli
38	119.5	2.9	2842	1	US-08-289-548A-7	Sequence 7, Appli
39	119.5	2.9	2842	1	US-08-452-654-7	Sequence 7, Appli
40	119.5	2.9	2842	4	US-08-449-731-7	Sequence 7, Appli
41	119.5	2.9	2843	1	US-07-741-940-2	Sequence 2, Appli
42	119.5	2.9	2843	1	US-08-289-548A-2	Sequence 2, Appli
43	119.5	2.9	2843	1	US-08-452-654-2	Sequence 2, Appli
44	119.5	2.9	2843	1	US-08-452-655B-2	Sequence 2, Appli
45	119.5	2.9	2843	1	US-08-452-655B-7	Sequence 7, Appli

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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 3, 2005, 09:03:56 ; Search time 149 Seconds

(without alignments)
10437.386 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 4167
Sequence: 1 attcggcacgaggtggaagt.....accaaaaaaaaaaaaaaaaaaaaaa 2345

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 2826744

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103621_22833/app_query.fasta_1.2
503

-DB=Published_Applications_AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09771312 @CGN_1_1_207 @runat_01042005_103621_22833
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2694	64.7	504	11	US-09-771-312-2	Sequence 2, Appli
2	1940	46.6	376	16	US-10-788-792-245	Sequence 245, App
3	529	12.7	320	11	US-09-771-312-5	Sequence 5, Appli
4	320.5	7.7	223	9	US-09-864-761-42782	Sequence 42782, A
5	320.5	7.7	223	14	US-10-029-386-33567	Sequence 33567, A
6	236.5	5.7	123	10	US-09-764-891-4335	Sequence 4335, Ap
7	188	4.5	313	15	US-10-424-599-174584	Sequence 174584,
8	181.5	4.4	564	15	US-10-425-114-71576	Sequence 71576, A
9	173	4.2	776	16	US-10-437-963-198660	Sequence 198660,
10	162.5	3.9	815	10	US-09-957-763-2	Sequence 2, Appli
11	162.5	3.9	815	10	US-09-957-763-4	Sequence 4, Appli
12	160.5	3.9	729	16	US-10-437-963-127682	Sequence 127682,
13	158.5	3.8	1462	14	US-10-287-218-17	Sequence 17, Appl
14	158.5	3.8	1462	16	US-10-408-765A-756	Sequence 756, App
15	158.5	3.8	1462	16	US-10-474-291-17	Sequence 17, Appl
16	157.5	3.8	1604	16	US-10-437-963-123905	Sequence 123905,
17	155.5	3.7	150	16	US-10-767-701-33562	Sequence 33562, A
18	154.5	3.7	643	15	US-10-427-224-13	Sequence 13, Appl
19	153.5	3.7	668	15	US-10-424-599-256096	Sequence 256096,
20	151	3.6	641	9	US-09-925-298-652	Sequence 652, App
21	151	3.6	641	14	US-10-102-806-652	Sequence 652, App
22	148.5	3.6	1577	15	US-10-369-493-6924	Sequence 6924, Ap
23	148.5	3.6	1577	15	US-10-369-493-6925	Sequence 6925, Ap
24	148.5	3.6	1577	15	US-10-369-493-6926	Sequence 6926, Ap
25	142	3.4	2515	15	US-10-276-774-2651	Sequence 2651, Ap
26	140	3.4	198	15	US-10-108-260A-4770	Sequence 4770, Ap
27	139.5	3.3	158	16	US-10-767-701-42233	Sequence 42233, A
28	139	3.3	788	9	US-09-879-957-30	Sequence 30, Appl
29	139	3.3	788	16	US-10-807-856-30	Sequence 30, Appl
30	139	3.3	813	16	US-10-437-963-120203	Sequence 120203,
31	138	3.3	42	11	US-09-771-312-6	Sequence 6, Appli
32	138	3.3	557	9	US-09-764-856-60	Sequence 60, Appl
33	138	3.3	557	11	US-09-764-856-60	Sequence 60, Appl
34	138	3.3	557	14	US-10-102-627-60	Sequence 60, Appl
35	136	3.3	910	15	US-10-425-114-54499	Sequence 54499, A
36	136	3.3	1134	13	US-10-001-873-50	Sequence 50, Appl
37	135	3.2	3051	15	US-10-144-194A-62	Sequence 62, Appl
38	134	3.2	446	9	US-09-764-856-70	Sequence 70, Appl
39	134	3.2	446	11	US-09-764-856-70	Sequence 70, Appl
40	134	3.2	446	14	US-10-102-627-70	Sequence 70, Appl
41	134	3.2	644	16	US-10-437-963-109393	Sequence 109393,
42	133.5	3.2	1564	15	US-10-144-198-2	Sequence 2, Appli
43	133.5	3.2	1564	15	US-10-144-198-4	Sequence 4, Appli
44	131.5	3.2	324	15	US-10-425-114-59181	Sequence 59181, A
45	131.5	3.2	341	15	US-10-424-599-256098	Sequence 256098,

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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 3, 2005, 08:19:20 ; Search time 44.5 Seconds
(without alignments)
10140.598 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 4167
Sequence: 1 attcggcaccgaggtggaagt.....accaaaaaaaaaaaaaaaaaa 2345

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103619_22728/app_query.fasta_1.2
503

-DB=PIR_79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312 @CGN_1_1_60 @runat_01042005_103619_22728 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

8						
Result	Query					
No.	Score	Match	Length	DB	ID	Description
1	177.5	4.3	1105	2	T47582	hypothetical prote
2	169	4.1	767	2	S63182	hypothetical prote
3	158.5	3.8	1403	1	A47328	natural killer cel
4	156	3.7	542	2	T46464	hypothetical prote
5	155.5	3.7	695	2	T40168	hypothetical prote
6	154.5	3.7	643	2	A96636	unknown protein, 7
7	152	3.6	669	2	T28754	hypothetical prote
8	148.5	3.6	1577	2	T19722	hypothetical prote
9	146	3.5	368	2	G88636	protein W09G12.7 [
10	146	3.5	2152	2	T45583	hypothetical prote
11	145	3.5	3498	2	T22330	hypothetical prote
12	140.5	3.4	699	2	I38073	nucleolar phosphop
13	138	3.3	775	2	T21259	hypothetical prote
14	137.5	3.3	539	2	T15256	hypothetical prote
15	136.5	3.3	896	2	D96556	hypothetical prote
16	135	3.2	552	2	T27191	hypothetical prote
17	134.5	3.2	954	2	E86174	protein F19P19.26
18	133.5	3.2	1672	2	T46237	hypothetical prote
19	133	3.2	705	2	D88536	acidic protein - C
20	133	3.2	705	2	S27786	acidic protein - C
21	133	3.2	943	2	A42681	centromere protein
22	133	3.2	2526	2	T20531	hypothetical prote
23	133	3.2	2738	2	E88320	protein F07A11.6 [
24	132	3.2	679	2	S48437	hypothetical prote
25	131.5	3.2	425	2	S55147	hypothetical prote
26	131.5	3.2	1150	2	T13824	LK6 protein kinase
27	130	3.1	608	2	T02299	hypothetical prote
28	129.5	3.1	2722	2	T20532	hypothetical prote
29	129	3.1	817	2	S53919	hypothetical prote
30	128.5	3.1	543	2	T27190	hypothetical prote
31	128.5	3.1	845	2	A45669	neurofilament trip
32	128	3.1	664	2	S60062	hevin precursor -
33	128	3.1	816	2	T19049	hypothetical prote
34	127.5	3.1	493	2	T02376	hypothetical prote
35	127.5	3.1	677	1	S09078	chromogranin B pre
36	127	3.0	763	2	T08929	hypothetical prote
37	127	3.0	786	2	T33856	hypothetical prote
38	127	3.0	963	2	T04002	hypothetical prote
39	126.5	3.0	390	2	T34137	hypothetical prote
40	126	3.0	598	2	B40713	cylicin I - human
41	126	3.0	1032	2	A57514	RNA helicase HEL11
42	125.5	3.0	1560	2	T42727	proliferation pote
43	125.5	3.0	2218	2	B84683	hypothetical prote
44	125	3.0	1274	2	A89959	hypothetical prote
45	125	3.0	1877	2	T21861	hypothetical prote

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 3, 2005, 05:51:15 ; Search time 214 Seconds
(without alignments)
11222.670 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 4167
Sequence: 1 attcggcacgaggtggaagt.....accaaaaaaaaaaaaaaaaaa 2345

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103619_22715/app_query.fasta_1.2
503

-DB=UniProt_03 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312 @CGN_1_1_320 @runat_01042005_103619_22715 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :, UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	2826	67.8	528	1 GPT2_HUMAN	Q9nw75 homo sapien
2	2394.5	57.5	527	1 GPT2_MOUSE	Q7tqc7 mus musculu
3	1622.5	38.9	375	2 Q9D3E7	Q9d3e7 mus musculu

4	1595	38.3	410	2	Q6AY15	Q6ay15	rattus norv
5	1140	27.4	216	2	Q6PIX0	Q6pix0	homo sapien
6	636.5	15.3	500	2	Q6ZPW9	Q6zpw9	mus musculu
7	627.5	15.1	482	2	Q6PE65	Q6pe65	mus musculu
8	593.5	14.2	482	2	Q9H3M3	Q9h3m3	homo sapien
9	566	13.6	408	2	Q8CD08	Q8cd08	mus musculu
10	565	13.6	408	2	Q9DA49	Q9da49	mus musculu
11	533.5	12.8	453	2	Q9NWQ4	Q9nwq4	homo sapien
12	530.5	12.7	351	2	Q6PEJ7	Q6pej7	homo sapien
13	530.5	12.7	354	2	Q9ULR8	Q9ulr8	homo sapien
14	514.5	12.3	107	2	Q9CSX3	Q9csx3	mus musculu
15	338	8.1	275	2	Q9NWH0	Q9nwh0	homo sapien
16	320.5	7.7	221	2	Q9ULA8	Q9ula8	homo sapien
17	199	4.8	928	2	Q6H4V9	Q6h4v9	oryza sativ
18	177.5	4.3	812	2	Q6C233	Q6c233	yarrowia li
19	177.5	4.3	1007	2	Q8VYR8	Q8vyr8	arabidopsis
20	177.5	4.3	1105	2	Q9M383	Q9m383	arabidopsis
21	173	4.2	663	2	Q80UY8	Q80uy8	mus musculu
22	173	4.2	742	2	Q6Z2C8	Q6z2c8	oryza sativ
23	172	4.1	1067	2	Q8BY32	Q8by32	m mus muscu
24	171	4.1	1067	2	Q8CH09	Q8ch09	mus musculu
25	169.5	4.1	781	2	Q9SF87	Q9sf87	arabidopsis
26	169	4.1	767	1	YNW4_YEAST	P53866	saccharomyc
27	167	4.0	470	2	Q8CFM0	Q8cfm0	mus musculu
28	162.5	3.9	749	2	Q6DDU9	Q6ddu9	xenopus lae
29	162.5	3.9	815	1	RBM5_HUMAN	P52756	homo sapien
30	162	3.9	520	2	Q99KV9	Q99kv9	mus musculu
31	162	3.9	815	2	Q91YE7	Q91ye7	mus musculu
32	158.5	3.8	1462	1	NKCR_HUMAN	P30414	homo sapien
33	158	3.8	1191	2	Q9XY3	Q9xyy3	dictyosteli
34	157.5	3.8	808	2	Q6BYP9	Q6byp9	debaryomyce
35	157.5	3.8	852	1	RBMA_RAT	P70501	rattus norv
36	157.5	3.8	853	2	Q8BTP8	Q8btp8	mus musculu
37	157.5	3.8	857	2	Q80U75	Q80u75	mus musculu
38	157.5	3.8	930	2	Q99KG3	Q99kg3	mus musculu
39	156.5	3.8	1208	2	Q7PNP6	Q7pnp6	anopheles g
40	156	3.7	542	2	Q9NTB1	Q9ntb1	homo sapien
41	156	3.7	852	2	Q9BTX0	Q9btx0	homo sapien
42	156	3.7	929	1	RBMA_HUMAN	P98175	homo sapien
43	156	3.7	930	2	Q9BTE4	Q9bte4	homo sapien
44	156	3.7	995	2	Q7Z3D7	Q7z3d7	homo sapien
45	155.5	3.7	695	2	O74363	O74363	schizosacch

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OM nucleic - nucleic search, using sw model

Run on: April 2, 2005, 23:06:48 ; Search time 10037 Seconds
 (without alignments)
 11320.861 Million cell updates/sec

Title: US-09-771-312-1
 Perfect score: 2345
 Sequence: 1 attcggcagcaggtggaagt.....accaaaaaaaaaaaaaaaaaa 2345

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:*
 1: gb_ba:*
 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2345	100.0	2345	6	AX206855	AX206855 Sequence
2	2319.2	98.9	2344	6	AX405697	AX405697 Sequence
3	2314.4	98.7	2338	6	BD155908	BD155908 Primer fo

4	2314.4	98.7	2338	6	AX876032	AX876032 Sequence
5	2314.4	98.7	2338	9	AK001114	AK001114 Homo sapi
6	1269	54.1	4537	10	BC054810	BC054810 Mus muscu
7	1176	50.1	4022	6	BD183390	BD183390 Novel gen
8	1172.8	50.0	3250	9	BC063474	BC063474 Homo sapi
9	1145.4	48.8	3189	9	BC042193	BC042193 Homo sapi
10	1026	43.8	1026	6	CQ720787	CQ720787 Sequence
11	1008.2	43.0	1021	9	AK024701	AK024701 Homo sapi
c 12	878	37.4	177654	2	AC025988	AC025988 Homo sapi
c 13	878	37.4	185148	9	AC096641	AC096641 Homo sapi
c 14	874.8	37.3	178229	2	AC009420	AC009420 Homo sapi
15	756.2	32.2	817	6	BD146304	BD146304 Primer fo
16	756.2	32.2	817	6	AX866242	AX866242 Sequence
c 17	718.6	30.6	135060	9	AL354659	AL354659 Human DNA
c 18	718.6	30.6	142908	2	AL513172	AL513172 Homo sapi
19	713.8	30.4	759	9	BC027719	BC027719 Homo sapi
20	686.8	29.3	1392	10	BC079232	BC079232 Rattus no
21	527.6	22.5	180315	10	AC107843	AC107843 Mus muscu
c 22	527.6	22.5	260404	10	AC110033	AC110033 Mus muscu
c 23	488	20.8	530	6	BD151813	BD151813 Primer fo
c 24	488	20.8	530	6	AX871751	AX871751 Sequence
25	488	20.8	254644	2	AC136836	AC136836 Rattus no
26	488	20.8	256511	2	AC135040	AC135040 Rattus no
c 27	488	20.8	262721	2	AC106265	AC106265 Rattus no
28	467	19.9	467	6	CQ683049	CQ683049 Sequence
29	448.4	19.1	469	6	AR413083	AR413083 Sequence
30	448.4	19.1	469	6	AX969917	AX969917 Sequence
31	448.4	19.1	469	6	BD108636	BD108636 EST and e
c 32	405.2	17.3	425	6	AX206857	AX206857 Sequence
33	386.4	16.5	445	6	CQ431223	CQ431223 Sequence
34	361.4	15.4	448	6	CQ422360	CQ422360 Sequence
35	348.2	14.8	64462	2	AC107950	AC107950 Homo sapi
36	316.8	13.5	407	6	CQ735676	CQ735676 Sequence
c 37	291.2	12.4	360	6	AX409847	AX409847 Sequence
38	216	9.2	66626	2	AC100660	AC100660 Mus muscu
c 39	216	9.2	202785	10	AC108796	AC108796 Mus muscu
40	191.8	8.2	308	6	CQ673353	CQ673353 Sequence
41	188.6	8.0	201	11	BV202345	BV202345 sqnm20884
42	181.2	7.7	208	6	BD058539	BD058539 Secreted
c 43	170	7.2	148801	5	BX004824	BX004824 Zebrafish
c 44	170	7.2	149784	2	BX005303	BX005303 Danio rer
c 45	163.6	7.0	69478	2	AC101461	AC101461 Mus muscu

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OM nucleic - nucleic search, using sw model

Run on: April 2, 2005, 21:36:18 ; Search time 1237 Seconds
(without alignments)
11222.145 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 2345

Sequence: 1 attcggcagcaggtggaagt.....accaaaaaaaaaaaaaaaaaa 2345

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match %	Length	DB	ID	Description
	1	2345	100.0	2345	5	AAS11663	Aas11663 Prostate
	2	2319.2	98.9	2344	6	ABN59701	Abn59701 Novel hum
	3	2314.8	98.7	2583	11	ACN91982	Acn91982 Breast ca
	4	2314.4	98.7	2338	4	AAH13916	Aah13916 Human cDN
	5	2314.4	98.7	2338	13	ADR99112	Adr99112 Hypotheti
	6	756.2	32.2	817	4	AAH04312	Aah04312 Human cDN
	7	726	31.0	1563	5	AAS72189	Aas72189 DNA encod
c	8	549.8	23.4	553	6	ABT10667	Abt10667 Human bre
c	9	488	20.8	530	4	AAH09821	Aah09821 Human cDN
c	10	405.2	17.3	425	5	AAS11664	Aas11664 84P2A9 su
	11	386.4	16.5	445	4	AAL23787	Aal23787 Human bre
	12	385.4	16.4	492	11	ACN84952	Acn84952 Breast ca
	13	382	16.3	382	6	ABK35967	Abk35967 cDNA sequ
	14	361.4	15.4	448	4	AAL14929	Aal14929 Human bre
c	15	291.2	12.4	360	6	ABN95996	Abn95996 Gene #249
	16	250.2	10.7	330	7	ADS72558	Ads72558 Human kid
	17	181.2	7.7	208	2	AAV86416	Aav86416 EST clone

18	121	5.2	1823	6	ABL53700	Ab153700 Human pho
19	121	5.2	2433	6	ABQ61016	Abq61016 14 clone
20	118.4	5.0	2434	6	ABN59974	Abn59974 Novel hum
21	116	4.9	1474	6	ABN59883	Abn59883 Novel hum
22	115.4	4.9	2112	4	AAH16534	Aah16534 Human cDN
23	113	4.8	1656	5	AAS87595	Aas87595 DNA encod
24	109.8	4.7	740	4	AAH03286	Aah03286 Human cDN
25	109.8	4.7	1851	4	AAH13673	Aah13673 Human cDN
26	99.8	4.3	371	4	AAL01647	Aal01647 Human rep
27	87	3.7	109	3	AAC12727	Aac12727 Human sec
28	85.4	3.6	747	2	AAZ16358	Aaz16358 Human gen
29	82	3.5	300	2	AAZ14849	Aaz14849 Human gen
30	64.8	2.8	321	5	ADL36721	Adl36721 Human ova
31	64.8	2.8	321	5	ADI71565	Adi71565 Human ova
32	64.8	2.8	390	5	ADL43105	Adl43105 Human ova
33	60	2.6	60	6	ABN33768	Abn33768 Human spl
34	57.8	2.5	673	4	AAI21087	Aai21087 Probe #11
35	57.8	2.5	673	4	ABA66165	Aba66165 Human foe
36	57.8	2.5	673	4	AAI46350	Aai46350 Probe #15
37	57.8	2.5	673	4	ABA48281	Aba48281 Human bre
38	57.8	2.5	673	4	AAK40330	Aak40330 Human bon
39	57.8	2.5	673	4	AAK14584	Aak14584 Human bra
40	57.8	2.5	673	4	ABS39901	Abs39901 Human liv
41	57.8	2.5	673	5	AAI06807	Aai06807 Probe #67
42	57.8	2.5	673	6	ABS14348	Abs14348 Human gen
43	57.8	2.5	673	12	ACH91528	Ach91528 Human gen
44	57.8	2.5	978	4	AAI11878	Aai11878 Probe #18
45	57.8	2.5	978	4	ABA53579	Aba53579 Human foe

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 00:18:03 ; Search time 394 Seconds
(without alignments)
9738.754 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 2345
Sequence: 1 attcggcaccgaggtggaagt.....accaaaaaaaaaaaaaaaaaa 2345

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query					
No.	Score	Match	Length	DB	ID	Description	
	1	448.4	19.1	469	4	US-09-621-976-720	Sequence 720, App
	2	87	3.7	109	4	US-09-513-999C-16802	Sequence 16802, A
c	3	78	3.3	7218	1	US-08-232-463-14	Sequence 14, Appl
c	4	47.2	2.0	1141	4	US-09-806-708B-22	Sequence 22, Appl
	5	46	2.0	41736	4	US-09-949-016-17091	Sequence 17091, A
c	6	45.6	1.9	42348	4	US-09-949-016-17157	Sequence 17157, A
	7	45.4	1.9	2327	4	US-10-066-130-20	Sequence 20, Appl
	8	45.4	1.9	2674	4	US-10-066-130-19	Sequence 19, Appl
	9	45.4	1.9	2771	4	US-10-066-130-18	Sequence 18, Appl
	10	45.4	1.9	5860	4	US-10-066-130-17	Sequence 17, Appl
c	11	45.4	1.9	12980	3	US-08-811-566-5	Sequence 5, Appli
c	12	45.4	1.9	12980	3	US-09-034-756-5	Sequence 5, Appli
c	13	44.8	1.9	191433	4	US-09-949-016-16144	Sequence 16144, A
	14	43.8	1.9	1141	4	US-09-806-708B-22	Sequence 22, Appl
	15	43.2	1.8	614	4	US-09-902-540-1318	Sequence 1318, Ap
c	16	42.6	1.8	45716	3	US-08-965-048-5	Sequence 5, Appli
c	17	42.6	1.8	45989	3	US-08-965-048-6	Sequence 6, Appli
	18	42.4	1.8	3275	3	US-09-370-838-151	Sequence 151, App
	19	42.4	1.8	3275	4	US-09-854-133-151	Sequence 151, App
	20	42.2	1.8	291	1	US-07-922-723A-7	Sequence 7, Appli
	21	42.2	1.8	291	1	US-07-799-828C-7	Sequence 7, Appli
	22	42.2	1.8	291	1	US-08-074-275-7	Sequence 7, Appli
	23	42.2	1.8	291	1	US-08-480-366-7	Sequence 7, Appli
	24	42.2	1.8	291	2	US-07-952-277A-7	Sequence 7, Appli
	25	42.2	1.8	612	4	US-09-902-540-1357	Sequence 1357, Ap
c	26	42.2	1.8	63804	4	US-09-949-016-15200	Sequence 15200, A
c	27	41.8	1.8	601	4	US-09-949-016-157832	Sequence 157832,
c	28	41.6	1.8	154023	4	US-09-949-016-17057	Sequence 17057, A
c	29	41.2	1.8	601	4	US-09-949-016-89635	Sequence 89635, A
c	30	41.2	1.8	601	4	US-09-949-016-89636	Sequence 89636, A
	31	41.2	1.8	1447	3	US-09-443-041A-27	Sequence 27, Appl
	32	41.2	1.8	2262	4	US-09-311-021-171	Sequence 171, App
c	33	41.2	1.8	23927	4	US-09-949-016-14284	Sequence 14284, A
c	34	41	1.7	601	4	US-09-949-016-193621	Sequence 193621,
	35	41	1.7	801	4	US-09-792-024-10	Sequence 10, Appl
	36	41	1.7	580073	4	US-08-545-528D-1	Sequence 1, Appli
	37	40.8	1.7	2223	1	US-08-257-073-4	Sequence 4, Appli
	38	40.8	1.7	168174	4	US-10-071-411A-63	Sequence 63, Appl
	39	40.8	1.7	168273	4	US-10-071-411A-2	Sequence 2, Appli

40	40.6	1.7	2608	4	US-09-904-615-16	Sequence 16, Appl
41	40.4	1.7	240	1	US-08-628-417-6	Sequence 6, Appli
42	40.4	1.7	1696	4	US-09-835-811-1	Sequence 1, Appli
43	40	1.7	1798	3	US-09-797-906-1	Sequence 1, Appli
44	40	1.7	49931	4	US-09-949-016-13727	Sequence 13727, A
45	40	1.7	49931	4	US-09-949-016-13728	Sequence 13728, A

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 03:39:00 ; Search time 1330 Seconds
(without alignments)
10671.499 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 2345
Sequence: 1 attcggcaccgaggtggaagt.....accaaaaaaaaaaaaaaaaaa 2345

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query				ID	Description
	No.	Score	Match	Length	DB			
	1	2345	100.0	2345	11	US-09-771-312-1		Sequence 1, Appli
	2	2314.8	98.7	2583	14	US-10-198-846-13132		Sequence 13132, A
	3	2314.4	98.7	2338	18	US-10-788-792-118		Sequence 118, App
	4	495.4	21.1	733	18	US-10-425-115-116525		Sequence 116525,
	5	467	19.9	467	17	US-10-242-535A-27975		Sequence 27975, A
	6	467	19.9	467	17	US-10-085-783A-27975		Sequence 27975, A
c	7	405.2	17.3	425	11	US-09-771-312-3		Sequence 3, Appli
	8	385.4	16.4	492	14	US-10-198-846-6102		Sequence 6102, Ap
	9	382	16.3	382	10	US-09-822-846-358		Sequence 358, App
c	10	291.2	12.4	360	9	US-09-880-107-2493		Sequence 2493, Ap
	11	250.2	10.7	330	15	US-10-102-524-1155		Sequence 1155, Ap
	12	191.8	8.2	308	17	US-10-242-535A-18279		Sequence 18279, A
	13	191.8	8.2	308	17	US-10-085-783A-18279		Sequence 18279, A
	14	128.6	5.5	418	13	US-10-027-632-284593		Sequence 284593,
	15	128.6	5.5	418	17	US-10-027-632-284593		Sequence 284593,
	16	99.8	4.3	371	10	US-09-764-891-1648		Sequence 1648, Ap
	17	93.4	4.0	171	9	US-09-783-590-5298		Sequence 5298, Ap
	18	64.8	2.8	321	10	US-09-814-353-4307		Sequence 4307, Ap
	19	64.8	2.8	321	10	US-09-814-353-10611		Sequence 10611, A
	20	64.8	2.8	390	10	US-09-814-353-16995		Sequence 16995, A
	21	60	2.6	60	10	US-09-908-975-6516		Sequence 6516, Ap
	22	57.8	2.5	673	9	US-09-864-761-26740		Sequence 26740, A
	23	57.8	2.5	673	16	US-10-029-386-24723		Sequence 24723, A
	24	57.8	2.5	978	9	US-09-864-761-10098		Sequence 10098, A
	25	52.6	2.2	496	17	US-10-424-599-74788		Sequence 74788, A
	26	50	2.1	464	10	US-09-918-995-4057		Sequence 4057, Ap
	27	49.8	2.1	1151	17	US-10-424-599-31742		Sequence 31742, A
	28	49.8	2.1	684187	18	US-10-367-094-71		Sequence 71, Appl
	29	49.6	2.1	373	17	US-10-242-535A-3209		Sequence 3209, Ap
	30	49.6	2.1	373	17	US-10-085-783A-3209		Sequence 3209, Ap
	31	49.6	2.1	2575	10	US-09-960-706-955		Sequence 955, App
	32	49.6	2.1	2575	10	US-09-873-319-624		Sequence 624, App
	33	49.6	2.1	3094	10	US-09-957-763-1		Sequence 1, Appli
	34	49.6	2.1	3094	10	US-09-957-763-3		Sequence 3, Appli
	35	48.6	2.1	627	18	US-10-021-323-9336		Sequence 9336, Ap
c	36	48.4	2.1	417	18	US-10-425-115-158260		Sequence 158260,
	37	48.2	2.1	1629	17	US-10-424-599-9786		Sequence 9786, Ap
c	38	48	2.0	407	18	US-10-437-963-67034		Sequence 67034, A
c	39	48	2.0	247461	18	US-10-322-281-131		Sequence 131, App
	40	47.8	2.0	467	18	US-10-021-323-6541		Sequence 6541, Ap
c	41	47.8	2.0	6668	15	US-10-311-455-1670		Sequence 1670, Ap
	42	47.4	2.0	501	18	US-10-357-930-59111		Sequence 59111, A
	43	47	2.0	2941	14	US-10-198-846-9874		Sequence 9874, Ap

44	46.4	2.0	1764	17	US-10-369-022-27	Sequence 27, Appl
45	46.4	2.0	1764	18	US-10-768-158-15	Sequence 15, Appl

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 00:13:53 ; Search time 7542 Seconds
(without alignments)
11835.151 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 2345
Sequence: 1 attcggcagcaggtggaagt.....accaaaaaaaaaaaaaaaaaa 2345

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1253.8	53.5	2746	3	AK029990	AK029990 Mus muscu
2	1185.6	50.6	3844	3	AK030026	AK030026 Mus muscu
3	1055.2	45.0	2234	3	AK053781	AK053781 Mus muscu

	4	930	39.7	1099	1	AL539463	AL539463	AL539463
	5	875.4	37.3	923	5	BX380890	BX380890	BX380890
	6	841.4	35.9	1565	3	AK017975	AK017975	Mus muscu
	7	816.8	34.8	1961	3	AK032734	AK032734	Mus muscu
	8	780.4	33.3	816	4	BG210260	BG210260	RST29795
	9	773.4	33.0	782	5	BX355142	BX355142	BX355142
c	10	766.6	32.7	837	5	BX415499	BX415499	BX415499
	11	756.2	32.2	817	1	AU120500	AU120500	AU120500
	12	755	32.2	785	4	BG212347	BG212347	RST31934
	13	752	32.1	890	4	BG196275	BG196275	RST15489
	14	746.4	31.8	770	7	CN365216	CN365216	170004247
c	15	712	30.4	895	4	BG189037	BG189037	RST8073 A
c	16	702.6	30.0	711	5	BQ001706	BQ001706	UI-H-DH1-
c	17	698.6	29.8	862	4	BG218714	BG218714	RST38455
	18	696.4	29.7	702	4	BI766808	BI766808	603056721
c	19	693	29.6	696	6	CB528650	CB528650	UI-H-FT2-
c	20	689.8	29.4	696	5	BM992124	BM992124	UI-H-DF1-
	21	686.4	29.3	3704	3	AK083471	AK083471	Mus muscu
	22	684.6	29.2	968	4	BG335967	BG335967	602404712
	23	678.6	28.9	790	5	BX415500	BX415500	BX415500
	24	678	28.9	678	5	BX955296	BX955296	DKFZp781N
c	25	674	28.7	694	5	BQ182986	BQ182986	UI-H-ED1-
	26	668.6	28.5	747	4	BG194707	BG194707	RST13873
c	27	666.4	28.4	676	4	BM683630	BM683630	UI-E-EJ1-
	28	661.2	28.2	667	5	BM929686	BM929686	UI-E-EJ1-
	29	642.8	27.4	675	4	BI560845	BI560845	603254011
c	30	642.2	27.4	659	6	CB046496	CB046496	NISC_gf04
c	31	633.8	27.0	849	4	BG190649	BG190649	RST9723 A
c	32	631.6	26.9	843	4	BG203931	BG203931	RST23324
	33	631.4	26.9	647	5	BU951125	BU951125	io76b05.y
	34	620.4	26.5	638	6	CB554977	CB554977	MMSP0041_
	35	620.4	26.5	777	2	BE549223	BE549223	601078779
	36	612.4	26.1	660	4	BM721009	BM721009	UI-E-EO0-
c	37	611	26.1	755	4	BG212348	BG212348	RST31935
c	38	609.8	26.0	621	2	AW976618	AW976618	EST388727
	39	593.2	25.3	752	7	CN365215	CN365215	170004240
	40	589.8	25.2	593	5	BX506191	BX506191	DKFZp686P
	41	576.4	24.6	600	4	BI712934	BI712934	id99a12.y
	42	573.8	24.5	760	7	CK460603	CK460603	930893 MA
c	43	572	24.4	572	4	BI791523	BI791523	id99a12.x
	44	567.2	24.2	572	5	BP203612	BP203612	BP203612
	45	563.4	24.0	583	5	BP349820	BP349820	BP349820

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OM protein - protein search, using sw model

Run on: April 3, 2005, 09:05:51 ; Search time 84 Seconds
(without alignments)
2320.562 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.....GFPLPKSTSATTPNAGKSA 504

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	2694	100.0	504	4	AAU06524	Aau06524 Prostate
2	2694	100.0	528	4	AAB92632	Aab92632 Human pro
3	2694	100.0	528	5	ABB97288	Abb97288 Novel hum
4	1808	67.1	376	8	ADR99239	Adr99239 Hypotheti
5	825.5	30.6	313	4	ABG08002	Abg08002 Novel hum
6	608.5	22.6	423	4	ABG23408	Abg23408 Novel hum
7	591.5	22.0	446	5	ABB75706	Abb75706 Human pho
8	588.5	21.8	482	5	ABP43772	Abp43772 14 clone
9	533.5	19.8	453	5	ABB97561	Abb97561 Novel hum

10	530.5	19.7	351	4	AAB94662	Aab94662	Human pro
11	530.5	19.7	351	5	ABB97470	Abb97470	Novel hum
12	338	12.5	275	4	AAB92468	Aab92468	Human pro
13	320.5	11.9	223	4	AAM15386	Aam15386	Peptide #
14	320.5	11.9	223	4	ABB34392	Abb34392	Peptide #
15	320.5	11.9	223	4	AAM27874	Aam27874	Peptide #
16	320.5	11.9	223	4	ABB29229	Abb29229	Peptide #
17	320.5	11.9	223	4	AAM67577	Aam67577	Human bon
18	320.5	11.9	223	4	AAM55182	Aam55182	Human bra
19	320.5	11.9	223	4	ABG49223	Abg49223	Human liv
20	320.5	11.9	223	4	AAM03148	Aam03148	Peptide #
21	320.5	11.9	223	5	ABG37168	Abg37168	Human pep
22	320.5	11.9	223	8	ABO59933	Abo59933	Human gen
23	236.5	8.8	123	4	AAM95677	Aam95677	Human rep
24	196	7.3	1038	7	ADC03412	Adc03412	Rice flow
25	167.5	6.2	767	6	ABR53431	Abr53431	Protein s
26	167.5	6.2	767	7	ADK64670	Adk64670	Disease t
27	164.5	6.1	554	3	AAG36165	Aag36165	Arabidops
28	164.5	6.1	652	3	AAG36164	Aag36164	Arabidops
29	164.5	6.1	781	3	AAG36163	Aag36163	Arabidops
30	162.5	6.0	815	5	AAG78388	Aag78388	Human H37
31	162.5	6.0	815	7	AAE38620	Aae38620	Human H37
32	162.5	6.0	815	7	AAE38621	Aae38621	Human H37
33	162.5	6.0	815	8	ADP23184	Adp23184	PRO polyp
34	162	6.0	381	2	AAY07056	Aay07056	Renal can
35	157.5	5.8	852	7	ADD45318	Add45318	Rat Prote
36	157.5	5.8	852	7	ADE56352	Ade56352	Rat Prote
37	156.5	5.8	573	4	ADM19760	Adm19760	Protein e
38	156	5.8	929	4	AAM78604	Aam78604	Human pro
39	156	5.8	930	8	ABM82400	Abm82400	Tumour-as
40	156	5.8	1041	4	AAM79588	Aam79588	Human pro
41	151	5.6	641	3	AAB58944	Aab58944	Breast an
42	148.5	5.5	962	4	ABG04842	Abg04842	Novel hum
43	148.5	5.5	1403	8	ADH09502	Adh09502	Human hos
44	148.5	5.5	1462	6	ABP58346	Abp58346	Human cel
45	148.5	5.5	1462	6	ABU05132	Abu05132	Human exp

ALIGNMENTS

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OM protein - protein search, using sw model

Run on: April 3, 2005, 09:24:37 ; Search time 26 Seconds
(without alignments)
1447.043 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALESSEQAR.....GFPLPKSTSATTTNAGKSA 504

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	534	19.8	124	4	US-09-621-976-4580	Sequence 4580, Ap
2	162.5	6.0	815	4	US-09-538-092-1196	Sequence 1196, Ap
3	156	5.8	929	4	US-09-538-092-1232	Sequence 1232, Ap
4	151.5	5.6	620	4	US-09-270-767-46214	Sequence 46214, A
5	148.5	5.5	1462	4	US-09-538-092-1043	Sequence 1043, Ap
6	147.5	5.5	362	4	US-09-270-767-42306	Sequence 42306, A
7	131.5	4.9	1564	4	US-10-144-198-2	Sequence 2, Appli
8	131.5	4.9	1564	4	US-10-144-198-4	Sequence 4, Appli
9	126.5	4.7	1402	4	US-09-248-796A-14503	Sequence 14503, A
10	126	4.7	598	4	US-09-538-092-1083	Sequence 1083, Ap
11	126	4.7	1400	4	US-09-764-176-7	Sequence 7, Appli
12	124.5	4.6	748	3	US-08-725-459B-24	Sequence 24, Appl
13	122	4.5	664	1	US-08-421-661-6	Sequence 6, Appli
14	120.5	4.5	1034	4	US-09-976-594-590	Sequence 590, App
15	119	4.4	733	3	US-08-725-459B-21	Sequence 21, Appl
16	118.5	4.4	1739	4	US-09-976-594-76	Sequence 76, Appl
17	118.5	4.4	1739	4	US-09-538-092-824	Sequence 824, App
18	118.5	4.4	1740	4	US-09-949-016-8860	Sequence 8860, Ap
19	118	4.4	769	3	US-08-725-459B-39	Sequence 39, Appl
20	117.5	4.4	621	4	US-09-248-796A-15807	Sequence 15807, A
21	117.5	4.4	810	3	US-09-540-824-25	Sequence 25, Appl
22	117.5	4.4	848	4	US-09-248-796A-18403	Sequence 18403, A
23	117	4.3	733	3	US-08-725-459B-22	Sequence 22, Appl
24	117	4.3	769	3	US-08-725-459B-37	Sequence 37, Appl
25	117	4.3	769	3	US-08-725-459B-38	Sequence 38, Appl
26	117	4.3	769	3	US-08-725-459B-40	Sequence 40, Appl
27	116.5	4.3	971	4	US-09-538-092-1332	Sequence 1332, Ap
28	116.5	4.3	1032	4	US-09-976-594-214	Sequence 214, App
29	116.5	4.3	1589	4	US-09-543-681A-4998	Sequence 4998, Ap
30	116.5	4.3	1969	4	US-09-418-710-72	Sequence 72, Appl

31	116.5	4.3	1969	4	US-09-839-479-71	Sequence 71, Appl
32	116.5	4.3	1972	4	US-09-418-710-21	Sequence 21, Appl
33	116.5	4.3	1972	4	US-09-839-479-21	Sequence 21, Appl
34	116	4.3	473	4	US-09-248-796A-15689	Sequence 15689, A
35	116	4.3	709	4	US-09-949-016-10367	Sequence 10367, A
36	115.5	4.3	1085	1	US-08-431-080-28	Sequence 28, Appl
37	115.5	4.3	1085	2	US-08-938-534-28	Sequence 28, Appl
38	115.5	4.3	1085	3	US-09-345-294-28	Sequence 28, Appl
39	115.5	4.3	2907	4	US-09-698-295-1	Sequence 1, Appli
40	115	4.3	664	4	US-09-917-254-78	Sequence 78, Appl
41	115	4.3	779	4	US-10-164-595-56	Sequence 56, Appl
42	115	4.3	968	3	US-09-302-812-6	Sequence 6, Appli
43	115	4.3	968	3	US-09-511-477-6	Sequence 6, Appli
44	115	4.3	968	3	US-09-511-507-6	Sequence 6, Appli
45	115	4.3	2842	1	US-07-741-940-7	Sequence 7, Appli

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OM protein - protein search, using sw model

Run on: April 3, 2005, 09:32:12 ; Search time 74 Seconds
(without alignments)
2258.416 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.....GFPLPKSTSATTPNAGKSA 504

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2694	100.0	504	11	US-09-771-312-2	Sequence 2, Appli
2	1808	67.1	376	16	US-10-788-792-245	Sequence 245, App
3	529	19.6	320	11	US-09-771-312-5	Sequence 5, Appli
4	320.5	11.9	223	9	US-09-864-761-42782	Sequence 42782, A
5	320.5	11.9	223	14	US-10-029-386-33567	Sequence 33567, A
6	236.5	8.8	123	10	US-09-764-891-4335	Sequence 4335, Ap
7	188	7.0	313	15	US-10-424-599-174584	Sequence 174584,
8	181.5	6.7	564	15	US-10-425-114-71576	Sequence 71576, A
9	169	6.3	776	16	US-10-437-963-198660	Sequence 198660,
10	162.5	6.0	815	10	US-09-957-763-2	Sequence 2, Appli
11	162.5	6.0	815	10	US-09-957-763-4	Sequence 4, Appli
12	159	5.9	729	16	US-10-437-963-127682	Sequence 127682,
13	155.5	5.8	150	16	US-10-767-701-33562	Sequence 33562, A
14	151	5.6	641	9	US-09-925-298-652	Sequence 652, App
15	151	5.6	641	14	US-10-102-806-652	Sequence 652, App
16	149	5.5	668	15	US-10-424-599-256096	Sequence 256096,
17	148.5	5.5	1462	14	US-10-287-218-17	Sequence 17, Appl
18	148.5	5.5	1462	16	US-10-408-765A-756	Sequence 756, App
19	148.5	5.5	1462	16	US-10-474-291-17	Sequence 17, Appl
20	145	5.4	1604	16	US-10-437-963-123905	Sequence 123905,
21	143	5.3	1577	15	US-10-369-493-6924	Sequence 6924, Ap
22	143	5.3	1577	15	US-10-369-493-6925	Sequence 6925, Ap
23	143	5.3	1577	15	US-10-369-493-6926	Sequence 6926, Ap
24	140	5.2	198	15	US-10-108-260A-4770	Sequence 4770, Ap
25	138.5	5.1	158	16	US-10-767-701-42233	Sequence 42233, A
26	138	5.1	42	11	US-09-771-312-6	Sequence 6, Appli
27	135.5	5.0	557	9	US-09-764-856-60	Sequence 60, Appl
28	135.5	5.0	557	11	US-09-764-856-60	Sequence 60, Appl
29	135.5	5.0	557	14	US-10-102-627-60	Sequence 60, Appl
30	135.5	5.0	643	15	US-10-427-224-13	Sequence 13, Appl
31	134	5.0	644	16	US-10-437-963-109393	Sequence 109393,
32	133	4.9	446	9	US-09-764-856-70	Sequence 70, Appl
33	133	4.9	446	11	US-09-764-856-70	Sequence 70, Appl
34	133	4.9	446	14	US-10-102-627-70	Sequence 70, Appl
35	131.5	4.9	324	15	US-10-425-114-59181	Sequence 59181, A
36	131.5	4.9	341	15	US-10-424-599-256098	Sequence 256098,
37	131.5	4.9	420	9	US-09-764-868-900	Sequence 900, App
38	131.5	4.9	1564	15	US-10-144-198-2	Sequence 2, Appli

39	131.5	4.9	1564	15	US-10-144-198-4	Sequence 4, Appli
40	130.5	4.8	1285	9	US-09-982-091A-2	Sequence 2, Appli
41	130	4.8	616	17	US-10-488-614-1	Sequence 1, Appli
42	130	4.8	616	17	US-10-488-608-1	Sequence 1, Appli
43	130	4.8	1424	16	US-10-437-963-160683	Sequence 160683,
44	129.5	4.8	645	17	US-10-488-614-3	Sequence 3, Appli
45	129.5	4.8	645	17	US-10-488-608-3	Sequence 3, Appli

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OM protein - protein search, using sw model

Run on: April 3, 2005, 09:23:11 ; Search time 26 Seconds
(without alignments)
1865.125 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALESSEQR.....GFPLPKSTSATTPNAGKSA 504

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	177.5	6.6	1105	2	T47582	hypothetical prote	
2	167.5	6.2	767	2	S63182	hypothetical prote	
3	156	5.8	542	2	T46464	hypothetical prote	
4	149	5.5	695	2	T40168	hypothetical prote	

5	148.5	5.5	1403	1	A47328	natural killer cel
6	146.5	5.4	669	2	T28754	hypothetical prote
7	143	5.3	1577	2	T19722	hypothetical prote
8	143	5.3	3498	2	T22330	hypothetical prote
9	138.5	5.1	368	2	G88636	protein W09G12.7 [
10	135.5	5.0	643	2	A96636	unknown protein, 7
11	134.5	5.0	699	2	I38073	nucleolar phosphop
12	134.5	5.0	896	2	D96556	hypothetical prote
13	133.5	5.0	1672	2	T46237	hypothetical prote
14	133	4.9	705	2	D88536	acidic protein - C
15	133	4.9	705	2	S27786	acidic protein - C
16	133	4.9	943	2	A42681	centromere protein
17	131.5	4.9	425	2	S55147	hypothetical prote
18	130	4.8	608	2	T02299	hypothetical prote
19	130	4.8	679	2	S48437	hypothetical prote
20	129.5	4.8	2526	2	T20531	hypothetical prote
21	129.5	4.8	2722	2	T20532	hypothetical prote
22	129.5	4.8	2738	2	E88320	protein F07A11.6 [
23	128.5	4.8	543	2	T27190	hypothetical prote
24	128.5	4.8	552	2	T27191	hypothetical prote
25	128.5	4.8	954	2	E86174	protein F19P19.26
26	127.5	4.7	493	2	T02376	hypothetical prote
27	127.5	4.7	539	2	T15256	hypothetical prote
28	127	4.7	763	2	T08929	hypothetical prote
29	127	4.7	786	2	T33856	hypothetical prote
30	127	4.7	845	2	A45669	neurofilament trip
31	127	4.7	963	2	T04002	hypothetical prote
32	126.5	4.7	390	2	T34137	hypothetical prote
33	126	4.7	598	2	B40713	cyclin I - human
34	126	4.7	1032	2	A57514	RNA helicase HEL11
35	125	4.6	1274	2	A89959	hypothetical prote
36	124.5	4.6	817	2	S53919	hypothetical prote
37	124	4.6	775	2	T21259	hypothetical prote
38	124	4.6	1166	2	H86341	hypothetical prote
39	123.5	4.6	849	2	E86306	Similar to tufteli
40	123	4.6	529	2	T50609	hypothetical prote
41	122	4.5	581	2	T22455	hypothetical prote
42	122	4.5	611	2	T22456	hypothetical prote
43	122	4.5	971	2	T24866	hypothetical prote
44	122	4.5	1230	2	T22458	hypothetical prote
45	121	4.5	4910	2	S64942	probable membrane

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OM protein - protein search, using sw model

Run on: April 3, 2005, 09:07:06 ; Search time 89 Seconds
(without alignments)
2899.864 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.....GFPLPKSTSATTPNAGKSA 504

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2694	100.0	528	1	GPT2_HUMAN	Q9nw75 homo sapien
2	2310	85.7	527	1	GPT2_MOUSE	Q7tqc7 mus musculu
3	1538	57.1	375	2	Q9D3E7	Q9d3e7 mus musculu
4	1513.5	56.2	410	2	Q6AY15	Q6ay15 rattus norv
5	1008	37.4	216	2	Q6PIX0	Q6pix0 homo sapien
6	627.5	23.3	482	2	Q6PE65	Q6pe65 mus musculu
7	627.5	23.3	500	2	Q6ZPW9	Q6zpw9 mus musculu
8	593.5	22.0	482	2	Q9H3M3	Q9h3m3 homo sapien
9	566	21.0	408	2	Q8CD08	Q8cd08 mus musculu
10	565	21.0	408	2	Q9DA49	Q9da49 mus musculu
11	533.5	19.8	453	2	Q9NWQ4	Q9nwq4 homo sapien
12	530.5	19.7	351	2	Q6PEJ7	Q6pej7 homo sapien
13	530.5	19.7	354	2	Q9ULR8	Q9ulr8 homo sapien
14	430	16.0	107	2	Q9CSX3	Q9csx3 mus musculu
15	338	12.5	275	2	Q9NWH0	Q9nwh0 homo sapien
16	320.5	11.9	221	2	Q9ULA8	Q9ula8 homo sapien
17	197	7.3	928	2	Q6H4V9	Q6h4v9 oryza sativ
18	177.5	6.6	1007	2	Q8VYR8	Q8vyr8 arabidopsis
19	177.5	6.6	1105	2	Q9M383	Q9m383 arabidopsis
20	170	6.3	812	2	Q6C233	Q6c233 yarrowia li
21	169	6.3	742	2	Q6Z2C8	Q6z2c8 oryza sativ
22	167.5	6.2	767	1	YNW4_YEAST	P53866 saccharomyc
23	164.5	6.1	470	2	Q8CFM0	Q8cfm0 mus musculu
24	164.5	6.1	663	2	Q80UY8	Q80uy8 mus musculu
25	164.5	6.1	781	2	Q9SF87	Q9sf87 arabidopsis
26	163.5	6.1	1067	2	Q8BY32	Q8by32 m mus muscu
27	162.5	6.0	815	1	RBM5_HUMAN	P52756 homo sapien
28	162.5	6.0	1067	2	Q8CH09	Q8ch09 mus musculu
29	162	6.0	520	2	Q99KV9	Q99kv9 mus musculu

30	162	6.0	815	2	Q91YE7	Q91ye7	mus	musculu
31	160.5	6.0	749	2	Q6DDU9	Q6ddu9	xenopus	lae
32	157.5	5.8	808	2	Q6BYP9	Q6byp9	debaryomyce	
33	157.5	5.8	852	1	RBMA_RAT	P70501	rattus	norv
34	157.5	5.8	853	2	Q8BTP8	Q8btp8	mus	musculu
35	157.5	5.8	857	2	Q80U75	Q80u75	mus	musculu
36	157.5	5.8	930	2	Q99KG3	Q99kg3	mus	musculu
37	156	5.8	542	2	Q9NTB1	Q9ntb1	homo	sapien
38	156	5.8	852	2	Q9BTX0	Q9btx0	homo	sapien
39	156	5.8	929	1	RBMA_HUMAN	P98175	homo	sapien
40	156	5.8	930	2	Q9BTE4	Q9bte4	homo	sapien
41	156	5.8	995	2	Q7Z3D7	Q7z3d7	homo	sapien
42	152.5	5.7	711	1	VG5Q_MOUSE	Q7tn31	mus	musculu
43	151.5	5.6	832	2	Q9VNC4	Q9vnc4	drosophila	
44	149.5	5.5	599	2	Q8MLA6	Q8mla6	drosophila	
45	149	5.5	695	2	O74363	O74363	schizosacch	

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 09:33:18 ; Search time 6454 Seconds
(without alignments)
3783.921 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALESSEQAR.....GFPLPKSTSATTTPNAGKSA 504

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103709_23798/app_query.fasta_1.6
47

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312_CGN_1_1_4200_@runat_01042005_103709_23798 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*

11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					Description
	No.	Score	Match	Length	ID	
	1	2694	100.0	2338	6	BD155908
	2	2694	100.0	2338	6	AX876032
	3	2694	100.0	2338	9	AK001114
	4	2694	100.0	2344	6	AX405697
	5	2694	100.0	2345	6	AX206855
	6	2318	86.0	4537	10	BC054810
	7	1813	67.3	1026	6	CQ720787
	8	1813	67.3	4022	6	BD183390
	9	1808	67.1	3189	9	BC042193
	10	1807	67.1	3250	9	BC063474
	11	1513.5	56.2	1392	10	BC079232
c	12	1229	45.6	135060	9	AL354659
c	13	1229	45.6	142908	2	AL513172
	14	1072.5	39.8	180315	10	AC107843
c	15	1072.5	39.8	260404	10	AC110033
	16	1054	39.1	817	6	BD146304
	17	1054	39.1	817	6	AX866242
	18	1038	38.5	254644	2	AC136836
	19	1038	38.5	256511	2	AC135040
c	20	1038	38.5	262721	2	AC106265
	21	1008	37.4	759	9	BC027719
	22	627.5	23.3	3947	10	BC058256
	23	627.5	23.3	4311	10	AK129299
	24	627.5	23.3	4314	10	BC050782
	25	608	22.6	1021	9	AK024701
c	26	566.5	21.0	148801	5	BX004824
c	27	566.5	21.0	149784	2	BX005303
	28	563.5	20.9	2434	6	AX405970
	29	563.5	20.9	2463	9	AK000696
	30	544	20.2	407	6	CQ735676
	31	534	19.8	469	6	AR413083
	32	534	19.8	469	6	AX969917
	33	534	19.8	469	6	BD108636
	34	530.5	19.7	1474	6	AX405879
	35	530.5	19.7	1485	9	BC058032
	36	530.5	19.7	2112	6	BD158526
	37	530.5	19.7	2112	6	AX880680
	38	530.5	19.7	2112	9	AK023523
	39	530.5	19.7	6256	9	AB032978
	40	422	15.7	1490	9	BC038835
	41	420	15.6	445	6	CQ431223
	42	417	15.5	849	5	CR523866
c	43	387	14.4	177654	2	AC025988

c	44	387	14.4	178229	2	AC009420	AC009420 Homo sapi
c	45	387	14.4	185148	9	AC096641	AC096641 Homo sapi

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 09:32:47 ; Search time 780 Seconds
(without alignments)
3825.064 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.....GFPLPKSTSATTPNAGKSA 504

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103709_23788/app_query.fasta_1.6
47

-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312 @CGN_1_1_644 @runat_01042005_103709_23788 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*

8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length				
1	2694	100.0	2338	4	AAH13916	Aah13916 Human cDN	
2	2694	100.0	2338	13	ADR99112	Adr99112 Hypotheti	
3	2694	100.0	2344	6	ABN59701	Abn59701 Novel hum	
4	2694	100.0	2345	5	AAS11663	Aas11663 Prostate	
5	2694	100.0	2583	11	ACN91982	Acn91982 Breast ca	
6	1495.5	55.5	1563	5	AAS72189	Aas72189 DNA encod	
7	1054	39.1	817	4	AAH04312	Aah04312 Human cDN	
c 8	967	35.9	553	6	ABT10667	Abt10667 Human bre	
9	600	22.3	1656	5	AAS87595	Aas87595 DNA encod	
10	591.5	22.0	1823	6	ABL53700	Abl53700 Human pho	
11	588.5	21.8	2433	6	ABQ61016	Abq61016 14 clone	
12	563.5	20.9	2434	6	ABN59974	Abn59974 Novel hum	
13	530.5	19.7	1474	6	ABN59883	Abn59883 Novel hum	
14	530.5	19.7	2112	4	AAH16534	Aah16534 Human cDN	
15	439	16.3	330	7	ADS72558	Ads72558 Human kid	
16	420	15.6	445	4	AAL23787	Aal23787 Human bre	
17	420	15.6	492	11	ACN84952	Acn84952 Breast ca	
18	377	14.0	448	4	AAL14929	Aal14929 Human bre	
19	348.5	12.9	1851	4	AAH13673	Aah13673 Human cDN	
20	321.5	11.9	740	4	AAH03286	Aah03286 Human cDN	
21	320.5	11.9	673	4	AAI21087	Aai21087 Probe #11	
22	320.5	11.9	673	4	ABA66165	Aba66165 Human foe	
23	320.5	11.9	673	4	AAI46350	Aai46350 Probe #15	
24	320.5	11.9	673	4	ABA48281	Aba48281 Human bre	
25	320.5	11.9	673	4	AAK40330	Aak40330 Human bon	
26	320.5	11.9	673	4	AAK14584	Aak14584 Human bra	
27	320.5	11.9	673	4	ABS39901	Abs39901 Human liv	
28	320.5	11.9	673	5	AAI06807	Aai06807 Probe #67	
29	320.5	11.9	673	6	ABS14348	Abs14348 Human gen	
30	320.5	11.9	673	12	ACH91528	Ach91528 Human gen	
31	313	11.6	978	4	AAI11878	Aai11878 Probe #18	
32	313	11.6	978	4	ABA53579	Aba53579 Human foe	
33	313	11.6	978	4	AAI33206	Aai33206 Probe #18	
34	313	11.6	978	4	ABA43160	Aba43160 Human bre	
35	313	11.6	978	4	AAK27304	Aak27304 Human bon	
36	313	11.6	978	4	AAK01845	Aak01845 Human bra	
37	313	11.6	978	4	ABS26879	Abs26879 Human liv	
38	313	11.6	978	5	AAI01816	Aai01816 Probe #18	
39	313	11.6	978	6	ABS01825	Abs01825 Human gen	
40	236.5	8.8	371	4	AAL01647	Aal01647 Human rep	
41	232	8.6	464	9	ACH16845	Ach16845 Human adu	

42	213.5	7.9	747	2	AAZ16358	Aaz16358 Human gen
43	200.5	7.4	300	2	AAZ14849	Aaz14849 Human gen
44	197	7.3	3117	10	ADC03411	Adc03411 Rice flow
45	189	7.0	382	6	ABK35967	Abk35967 cDNA sequ

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 09:37:13 ; Search time 255 Seconds
(without alignments)
3234.053 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALESSEQAR.....GFPLPKSTSATTPNAGKSA 504

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103710_23824/app_query.fasta_1.6
47

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312 @CGN_1_1_177 @runat_01042005_103710_23824 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
	1	534	19.8	469	4	US-09-621-976-720	Sequence 720, App
c	2	164.5	6.1	1200	4	US-09-270-767-10714	Sequence 10714, A
	3	164.5	6.1	1863	4	US-09-270-767-14647	Sequence 14647, A
c	4	146	5.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	5	146	5.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	6	136	5.0	2131	4	US-09-270-767-10558	Sequence 10558, A
c	7	134.5	5.0	2132	4	US-09-270-767-12419	Sequence 12419, A
	8	134.5	5.0	6088	4	US-09-620-312D-190	Sequence 190, App
	9	134.5	5.0	6316	4	US-09-976-594-974	Sequence 974, App
	10	134	5.0	6775	4	US-09-620-312D-289	Sequence 289, App
	11	133	4.9	43804	3	US-09-171-461-1	Sequence 1, Appli
	12	133	4.9	43804	4	US-09-970-711-1	Sequence 1, Appli
	13	132	4.9	1307	4	US-09-023-655-293	Sequence 293, App
	14	132	4.9	4209	4	US-09-248-796A-400	Sequence 400, App
	15	131.5	4.9	6429	4	US-10-144-198-3	Sequence 3, Appli
	16	131.5	4.9	6726	4	US-10-144-198-1	Sequence 1, Appli
	17	131	4.9	2040	4	US-09-614-221A-396	Sequence 396, App
	18	128.5	4.8	4773	4	US-09-270-767-14129	Sequence 14129, A
	19	127.5	4.7	1269	4	US-09-489-039A-979	Sequence 979, App
c	20	127.5	4.7	1425	4	US-09-489-039A-1173	Sequence 1173, Ap
c	21	127.5	4.7	4265	3	US-09-061-709-1	Sequence 1, Appli
c	22	127.5	4.7	4265	4	US-09-899-651-1	Sequence 1, Appli
c	23	127.5	4.7	4265	4	US-09-392-714-15	Sequence 15, Appl
c	24	127.5	4.7	4265	4	US-09-270-437D-1	Sequence 1, Appli
c	25	127.5	4.7	109690	4	US-09-949-016-13525	Sequence 13525, A
c	26	126.5	4.7	4031	2	US-08-993-118-1	Sequence 1, Appli
c	27	126.5	4.7	4031	3	US-08-845-528C-1	Sequence 1, Appli
c	28	126.5	4.7	4031	4	US-09-066-281B-1	Sequence 1, Appli
c	29	126.5	4.7	4031	4	US-09-468-433C-1	Sequence 1, Appli
c	30	126.5	4.7	4225	2	US-08-993-118-9	Sequence 9, Appli
c	31	126.5	4.7	4225	3	US-08-845-528C-9	Sequence 9, Appli
c	32	126.5	4.7	4225	4	US-09-066-281B-9	Sequence 9, Appli
c	33	126.5	4.7	4225	4	US-09-468-433C-9	Sequence 9, Appli
	34	126.5	4.7	6755	3	US-08-931-999-4	Sequence 4, Appli
	35	124.5	4.6	6158	4	US-09-799-451-897	Sequence 897, App
	36	124.5	4.6	12658	4	US-08-956-171E-127	Sequence 127, App
	37	124.5	4.6	12658	4	US-08-781-986A-127	Sequence 127, App
	38	124	4.6	6222	4	US-09-774-528-114	Sequence 114, App
	39	123.5	4.6	3238	4	US-09-949-016-740	Sequence 740, App
	40	123.5	4.6	3238	4	US-09-949-016-5546	Sequence 5546, Ap
	41	123.5	4.6	7600	4	US-09-469-211A-1	Sequence 1, Appli
	42	123	4.6	2302	4	US-09-620-312D-915	Sequence 915, App
	43	123	4.6	2443	4	US-09-949-016-1857	Sequence 1857, Ap
	44	122.5	4.5	1800	1	US-08-139-937-11	Sequence 11, Appl
	45	122.5	4.5	1800	5	PCT-US93-11310-11	Sequence 11, Appl

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 11:43:19 ; Search time 828 Seconds
(without alignments)
3684.126 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.....GFPLPKSTSATTTNAGKSA 504

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103711_23911/app_query.fasta_1.6
47

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09771312_@CGN_1_1_697_@runat_01042005_103711_23911
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB		ID	Description
No.	Score	Match	Length	DB	ID			
1	2694	100.0	2338	18	US-10-788-792-118			Sequence 118, App
2	2694	100.0	2345	11	US-09-771-312-1			Sequence 1, Appli
3	2694	100.0	2583	14	US-10-198-846-13132			Sequence 13132, A
4	874	32.4	733	18	US-10-425-115-116525			Sequence 116525,
5	439	16.3	330	15	US-10-102-524-1155			Sequence 1155, Ap
6	420	15.6	492	14	US-10-198-846-6102			Sequence 6102, Ap
7	374	13.9	467	17	US-10-242-535A-27975			Sequence 27975, A
8	374	13.9	467	17	US-10-085-783A-27975			Sequence 27975, A
9	320.5	11.9	673	9	US-09-864-761-26740			Sequence 26740, A
10	320.5	11.9	673	16	US-10-029-386-24723			Sequence 24723, A
11	313	11.6	978	9	US-09-864-761-10098			Sequence 10098, A
12	236.5	8.8	371	10	US-09-764-891-1648			Sequence 1648, Ap
13	232	8.6	464	10	US-09-918-995-4057			Sequence 4057, Ap
14	189	7.0	382	10	US-09-822-846-358			Sequence 358, App
15	188	7.0	2540	18	US-10-425-115-137446			Sequence 137446,
16	181.5	6.7	1845	17	US-10-425-114-33626			Sequence 33626, A
17	180.5	6.7	1151	17	US-10-424-599-31742			Sequence 31742, A
18	178	6.6	2331	18	US-10-437-963-96177			Sequence 96177, A
19	174.5	6.5	2980	18	US-10-425-115-57818			Sequence 57818, A
20	162.5	6.0	2575	10	US-09-960-706-955			Sequence 955, App
21	162.5	6.0	2575	10	US-09-873-319-624			Sequence 624, App
22	162.5	6.0	3094	10	US-09-957-763-1			Sequence 1, Appli
23	162.5	6.0	3094	10	US-09-957-763-3			Sequence 3, Appli
24	162	6.0	2208	9	US-09-925-298-234			Sequence 234, App
25	162	6.0	2208	14	US-10-102-806-234			Sequence 234, App
26	159	5.9	2714	18	US-10-437-963-25199			Sequence 25199, A
27	155.5	5.8	539	18	US-10-767-701-1998			Sequence 1998, Ap
28	150.5	5.6	1076	18	US-10-425-115-57819			Sequence 57819, A
29	150	5.6	171	9	US-09-783-590-5298			Sequence 5298, Ap
c 30	148.5	5.5	1990	9	US-09-864-761-4529			Sequence 4529, Ap
31	148.5	5.5	7058	16	US-10-287-218-38			Sequence 38, Appl
32	148.5	5.5	7058	18	US-10-474-291-38			Sequence 38, Appl
c 33	146	5.4	1683	9	US-09-712-363-13			Sequence 13, Appl
c 34	145	5.4	4950	18	US-10-437-963-21422			Sequence 21422, A
c 35	144.5	5.4	1655	9	US-09-764-856-38			Sequence 38, Appl

c	36	144.5	5.4	1655	11	US-09-764-856-38	Sequence 38, Appl
c	37	144.5	5.4	1655	14	US-10-102-627-38	Sequence 38, Appl
c	38	143.5	5.3	1960	9	US-09-864-761-4620	Sequence 4620, Ap
	39	143.5	5.3	3727	15	US-10-171-581-49	Sequence 49, Appl
	40	143	5.3	2995	17	US-10-424-599-113254	Sequence 113254,
	41	142.5	5.3	1938	15	US-10-106-698-1570	Sequence 1570, Ap
	42	142.5	5.3	2272	10	US-09-946-374-307	Sequence 307, App
	43	142.5	5.3	2272	13	US-10-052-586-345	Sequence 345, App
	44	142.5	5.3	2272	14	US-10-174-590-345	Sequence 345, App
	45	142.5	5.3	2272	14	US-10-176-758-345	Sequence 345, App

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 09:36:48 ; Search time 4719 Seconds
(without alignments)
4065.351 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.....GFPLPKSTSATTPNAGKSA 504

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103709_23808/app_query.fasta_1.6
47
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312@cgn_1_1_4352@runat_01042005_103709_23808 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query		Match Length DB		ID	Description
No.	Score	Match	Length	DB	ID		
1	2301	85.4	3844	3	AK030026		AK030026 Mus muscu
2	2275	84.4	2746	3	AK029990		AK029990 Mus muscu
3	2089.5	77.6	2234	3	AK053781		AK053781 Mus muscu
4	1614	59.9	1961	3	AK032734		AK032734 Mus muscu
5	1541	57.2	1565	3	AK017975		AK017975 Mus muscu
6	1389	51.6	1099	1	AL539463		AL539463 AL539463
7	1338	49.7	770	7	CN365216		CN365216 170004247
8	1303	48.4	3704	3	AK083471		AK083471 Mus muscu
9	1209	44.9	968	4	BG335967		BG335967 602404712
10	1200	44.5	923	5	BX380890		BX380890 BX380890
11	1179	43.8	790	5	BX415500		BX415500 BX415500
12	1108	41.1	756	7	CN457551		CN457551 UI-M-HN0-
13	1100	40.8	782	5	BX355142		BX355142 BX355142
14	1054	39.1	817	1	AU120500		AU120500 AU120500
15	1040	38.6	593	5	BX506191		BX506191 DKFZp686P
c 16	1008	37.4	676	4	BM683630		BM683630 UI-E-EJ1-
c 17	998	37.0	659	6	CB046496		CB046496 NISC_gf04
18	997.5	37.0	716	2	BB654618		BB654618 BB654618
c 19	988	36.7	555	5	BU952562		BU952562 io76b05.x
c 20	988	36.7	560	7	CK820603		CK820603 id99a12.y
c 21	988	36.7	725	1	AJ731509		AJ731509 AJ731509
c 22	984	36.5	572	4	BI791523		BI791523 id99a12.x
23	983.5	36.5	760	7	CK460603		CK460603 930893 MA
24	981	36.4	813	7	CK633792		CK633792 UI-M-HN0-
25	979	36.3	702	4	BI766808		BI766808 603056721
c 26	974	36.2	547	1	AI694727		AI694727 we42c09.x
27	972	36.1	880	7	CK600754		CK600754 AGENCOURT
28	968	35.9	678	5	BX955296		BX955296 DKFZp781N
c 29	967	35.9	553	1	AI949698		AI949698 wq13h04.x
c 30	965	35.8	542	2	BE501500		BE501500 hw32h06.x
31	941	34.9	667	5	BM929686		BM929686 UI-E-EJ1-
32	919	34.1	638	6	CB554977		CB554977 MMSP0041_
33	915	34.0	778	7	CO431345		CO431345 UI-M-HX0-
34	882.5	32.8	791	5	BU480355		BU480355 603842912
35	881	32.7	675	4	BI560845		BI560845 603254011
36	872.5	32.4	712	5	BP148863		BP148863 BP148863

	37	860	31.9	717	7	CN535149	CN535149	UI-M-HS0-
c	38	858	31.8	489	1	AI436121	AI436121	ti15f01.y
	39	856	31.8	647	5	BU951125	BU951125	io76b05.y
c	40	837	31.1	536	4	BG063093	BG063093	H3002A11-
c	41	835	31.0	537	4	BG063094	BG063094	H3002A12-
	42	833	30.9	624	1	AJ731494	AJ731494	AJ731494
	43	828.5	30.8	812	7	CR442142	CR442142	CR442142
	44	817	30.3	667	2	BB623181	BB623181	BB623181
	45	810	30.1	633	6	CD349992	CD349992	UI-M-FY0-